

# SEQUENCE LISTING

<110> YAN, Chunhua et al.

<120> ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
THEREOF

<130> CL000612DIVII

<140> To Be Assigned

<151> 2003-09-25

<150> 09/734,030

<151> 2000-12-12

<150> 60/207,281

<151> 2000-05-30

<160> 3

<170> FastSEQ for Windows Version 4.0

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<212> DNA

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| gccccgccgtc | cccggagccc  | tcggcgcccc  | gctgagcccc  | cgatcacttc  | ctccctgtga  | 180  |
| ccaaccggcg  | ctgcagggtta | gagcctggca  | atgccgtttg  | ggtgtgtgac  | tctgggcgac  | 240  |
| aagaagaact  | ataaccagcc  | atcggagggtg | actgacagat  | atgatttggg  | acaggtcac   | 300  |
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| acccgcaagg  | agtactttat  | cttcctggag  | ctggccacgg  | ggagggagggt | gtttgactgg  | 540  |
| atcctggacc  | agggctacta  | ctcggagcga  | gacacaagca  | acgtggtacg  | gcaagtcctg  | 600  |
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| gcttctgata  | agaacatcaa  | ggatgggtgtc | tgtgcccaga  | ttgaaaagaa  | ctttgccagg  | 1140 |
| gccaaagtga  | agaaggctgt  | ccgagtgacc  | accctcatga  | aacggctccg  | ggcaccagag  | 1200 |
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| tgtgtgccta | ctgaacctgg  | caaataaaca | tcaccctgca | aagccaaaaa | aaaaaaaaaa | 3060 |
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<213> Homo sapiens

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| Met | Pro | Phe | Gly | Cys | Val | Thr | Leu | Gly | Asp | Lys | Lys | Asn | Tyr | Asn | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Glu | Val | Thr | Asp | Arg | Tyr | Asp | Leu | Gly | Gln | Val | Ile | Lys | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Phe | Cys | Glu | Ile | Phe | Arg | Ala | Lys | Asp | Lys | Thr | Thr | Gly | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | His | Thr | Cys | Lys | Lys | Phe | Gln | Lys | Arg | Asp | Gly | Arg | Lys | Val | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ala | Ala | Lys | Asn | Glu | Ile | Gly | Ile | Leu | Lys | Met | Val | Lys | His | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Ile | Leu | Gln | Leu | Val | Asp | Val | Phe | Val | Thr | Arg | Lys | Glu | Tyr | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Phe | Leu | Glu | Leu | Ala | Thr | Gly | Arg | Glu | Val | Phe | Asp | Trp | Ile | Leu |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asp | Gln | Gly | Tyr | Tyr | Ser | Glu | Arg | Asp | Thr | Ser | Asn | Val | Val | Arg | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Val | Leu | Glu | Ala | Val | Ala | Tyr | Leu | His | Ser | Leu | Lys | Ile | Val | His | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Leu | Lys | Leu | Glu | Asn | Leu | Val | Tyr | Tyr | Asn | Arg | Leu | Lys | Asn | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Ile | Val | Ile | Ser | Asp | Phe | His | Leu | Ala | Lys | Leu | Glu | Asn | Gly | Leu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

Ile Lys Glu Pro Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Val  
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 Gly Arg Gln Arg Tyr Gly Arg Pro Val Asp Cys Trp Ala Ile Gly Val  
 195 200 205  
 Ile Met Tyr Ile Leu Leu Ser Gly Asn Pro Pro Phe Tyr Glu Glu Val  
 210 215 220  
 Glu Glu Asp Asp Tyr Glu Asn His Asp Lys Asn Leu Phe Arg Lys Ile  
 225 230 235 240  
 Leu Ala Gly Asp Tyr Glu Phe Asp Ser Pro Tyr Trp Asp Asp Ile Ser  
 245 250 255  
 Gln Ala Ala Lys Asp Leu Val Thr Arg Leu Met Glu Val Glu Gln Asp  
 260 265 270  
 Gln Arg Ile Thr Ala Glu Glu Ala Ile Ser His Glu Trp Ile Ser Gly  
 275 280 285  
 Asn Ala Ala Ser Asp Lys Asn Ile Lys Asp Gly Val Cys Ala Gln Ile  
 290 295 300  
 Glu Lys Asn Phe Ala Arg Ala Lys Trp Lys Lys Ala Val Arg Val Thr  
 305 310 315 320  
 Thr Leu Met Lys Arg Leu Arg Ala Pro Glu Gln Ser Ser Thr Ala Ala  
 325 330 335  
 Ala Gln Ser Ala Ser Ala Thr Asp Thr Ala Thr Pro Gly Ala Ala Gly  
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 Gly Ala Thr Ala Ala Ala Ala Ser Gly Ala Thr Ser Ala Pro Glu Gly  
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 Asp Ala Ala Arg Ala Ala Lys Ser Asp Asn Val Ala Pro Ala Asp Arg  
 370 375 380  
 Ser Ala Thr Pro Ala Thr Asp Gly Ser Ala Thr Pro Ala Thr Asp Gly  
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 Ser Val Thr Pro Ala Thr Asp Gly Ser Ile Thr Pro Ala Thr Asp Gly  
 405 410 415  
 Ser Val Thr Pro Val Thr Asp Arg Ser Ala Thr Pro Ala Thr Asp Gly  
 420 425 430  
 Arg Ala Thr Pro Ala Thr Glu Glu Ser Thr Val Pro Thr Thr Gln Ser  
 435 440 445  
 Ser Ala Met Leu Ala Thr Lys Ala Ala Ala Thr Pro Glu Pro Ala Met  
 450 455 460  
 Ala Gln Pro Asp Ser Thr Ala Pro Glu Gly Ala Thr Gly Gln Ala Pro  
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| cagtgggtgag | tgactgcagt | gttggggccc | ggtgtttgcc | cg         |            | 7542 |